SEQUENCE LISTING

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Heinrikson, Robert L.

<120> SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY

<130> 29915/00281

<140> 60/219,795
<141> 2000-07-19

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<170> PatentIn Ver. 2.0

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         35                  40                  45

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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
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Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
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Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
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Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
                405                 410                 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
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Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
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Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
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Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
         35                  40                  45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
     50                  55                  60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65                  70                  75                  80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                 85                  90                  95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
            100                 105                 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115                 120                 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
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Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
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Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
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Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
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Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
            260                 265                 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
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Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
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Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
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Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385                 390                 395                 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
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Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
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Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
        435                 440                 445

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
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<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 45
Asp Ala Ala His Pro Gly
1 5

<210> 46
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 46
Lys Val Glu Ala Asn Tyr Asp Val Glu Gly Glu Arg Lys Lys
1 5 10

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 47
Lys Val Glu Ala Asn Leu Ala Val Glu Gly Glu Arg Lys Lys
1 5 10

<210> 48
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 48
Lys Val Glu Ala Leu Tyr Ala Val Glu Gly Glu Arg Lys Lys
1 5 10

<210> 49
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<223> Xaa = E, G, I, D, T, cysteic acid or S

<400> 49
Xaa Ala Asn Tyr Glu Val Glu Phe
1 5

<210> 50
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
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<222> (2)
<223> Xaa= A, V, I, S, H, Y, T or F

<400> 50
Glu Xaa Asn Tyr Glu Val Glu Phe
1 5

<210> 51
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
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<222> (3)
<223> Xaa= N, L, K, S, G, T, D, A, Q, or E

<400> 51
Glu Ala Xaa Tyr Glu Val Glu Phe
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
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<400> 52
Glu Ala Asn Xaa Glu Val Glu Phe
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<210> 53
<211> 8
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

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<222> (5)
<223> Xaa= E, A, D, M, Q, S or G

<400> 53
Glu Ala Asn Tyr Xaa Val Glu Phe
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<210> 54
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
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<223> Xaa= V, A, N, T, L, F or S

<400> 54
Glu Ala Asn Tyr Glu Xaa Glu Phe
1 5

<210> 55

<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
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<223> Xaa= E, G, F, H, cysteic acid or S

<400> 55
Glu Ala Asn Tyr Glu Val Xaa Phe
1 5

<210> 56
<211> 8
<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

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<400> 56
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1 5

<210> 57
<211> 8
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<220>
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<400> 57
Xaa Val Leu Leu Ala Ala Gly Trp
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<210> 58
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peptide sequence

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<400> 58
Gly Xaa Leu Leu Ala Ala Gly Trp
1 5

<210> 59
<211> 8
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<220>
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<220>
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<400> 59
Gly Val Xaa Leu Ala Ala Gly Trp
1 5

<210> 60
<211> 8
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<220>
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<400> 60
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<210> 61
<211> 8
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<220>
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<220>
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<222> (5)
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<400> 61
Gly Val Leu Leu Xaa Ala Gly Trp
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<210> 62
<211> 8
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<220>
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<220>
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<400> 62
Gly Val Leu Leu Ala Xaa Gly Trp
1 5

<210> 63
<211> 8
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<220>
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<400> 63
Gly Val Leu Leu Ala Ala Xaa Trp
1 5

<210> 64
<211> 8
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<220>
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<220>
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<223> Xaa= F, W, G, A, H, P, G, N or S

<400> 64
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<210> 65

<211> 8
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<400> 65
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<210> 66
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<220>
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<220>
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<400> 66
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1 5

<210> 67
<211> 8
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<400> 67
Ile Ile Xaa Met Asp Asn Phe Gly
1 5

<210> 68
<211> 8
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peptide sequence

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<223> Xaa= Y, L, M, Nle, F or H

<400> 68
Ile Ile Lys Xaa Asp Asn Phe Gly
1 5

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<223> Xaa= E, A, D, M, Q, S or G

<400> 69

Ile Ile Lys Met Xaa Asn Phe Gly
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<210> 70
<211> 8
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<400> 70
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<210> 71
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<210> 72
<211> 8
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<400> 72
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1 5

<210> 73
<211> 10
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<400> 73
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<210> 74
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<210> 75
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<400> 75
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1 5 10

<210> 76
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<220>
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<223> Xaa= Y, L, M, Nle, F or H

<400> 76
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1 5

<210> 77
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1 5 10

<210> 78
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<223> Description of Artificial Sequence: synthetic peptide sequence

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1 5 10

<210> 79
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<210> 80
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<210> 81
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<400> 81
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1 5

<210> 82
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<400> 82
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<210> 83
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<400> 83
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<210> 84
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1 5

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<210> 87
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<210> 88
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<210> 91
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1 5

<210> 92
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<210> 93
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1 5

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1 5

<210> 102
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1 5

<210> 103
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<222> (7)
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<210> 104
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Xaa Phe Ala Xaa Xaa Xaa Xaa Asn
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1 5

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<210> 108
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Xaa Phe Ala Xaa Xaa Xaa Xaa Asn
1 5

<210> 109
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> SITE
<222> (1)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (4)
<223> Xaa = any amino acid

<220>
<221> SITE
<222> (5)
<223> Xaa= E, A, D, M, Q, S or G

<220>
<221> SITE
<222> (6)..(7)
<223> Xaa= any amino acid

<400> 109
Xaa Phe Ala Xaa Xaa Xaa Xaa Asn
1 5

<210> 110
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> SITE
<222> (1)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (4)..(5)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (6)
<223> Xaa= V, A, N, T, L, F or S

<220>
<221> SITE
<222> (7)
<223> Xaa= any amino acid

<400> 110
Xaa Phe Ala Xaa Xaa Xaa Xaa Asn
1 5

<210> 111
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> SITE
<222> (1)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (4)..(6)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (7)
<223> Xaa= E, G, F, H, cysteic acid or S

<400> 111
Xaa Phe Ala Xaa Xaa Xaa Xaa Asn
1 5

<210> 112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> SITE
<222> (1)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (4)..(7)
<223> Xaa= any amino acid

<220>
<221> SITE
<222> (8)
<223> Xaa= F, W, G, A, H, P, G, N or S

<400> 112
Xaa Phe Ala Xaa Xaa Xaa Xaa Xaa
1 5

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 113
Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5

<210> 114
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 114
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 115
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 115
Ala Cys Gly Ser Glu Ser Met Asp Ser Gly Ile Ser Leu Asp Asn Lys
1 5 10 15

Trp

<210> 116
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 116
Trp Lys Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Lys
1 5 10 15

Lys

<210> 117

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 117
Ala Asn Leu Ser Thr Phe Ala Gln Pro Arg Arg
1 5 10

<210> 118
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 118
Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe Ser Ser Val Glu Lys Leu
1 5 10 15

Leu His Leu Gly Gly Cys
20

<210> 119
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 119
Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe Ser Ser Val Glu Lys Leu
1 5 10 15

Leu His Leu Gly Gly Cys
20

<210> 120
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 120
Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
1 5 10

<210> 121
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> SITE
<222> (9)
<223> Xaa= cysteic acid

<400> 121
Val Glu Ala Leu Tyr Leu Val Cys Xaa Gly Glu Arg
1 5 10

<210> 122
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 122
Val Glu Ala Leu Tyr Leu Val Glu Gly Glu Arg
1 5 10

<210> 123
<211> 363
<212> PRT
<213> Homo sapiens

<220>
<223> galactosyltransferase

<400> 123
Met Ala Ser Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Cys Gly Ser
1 5 10 15

Ala Ile Gly Phe Leu Leu Cys Ser Gln Leu Phe Ser Ile Leu Leu Gly
20 25 30

Glu Lys Val Asp Thr Gln Pro Asn Val Leu His Asn Asp Pro His Ala
35 40 45

Arg His Ser Asp Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn
50 55 60

Phe Asn Ala Asp Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala
65 70 75 80

Glu Asn Leu Tyr Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly
85 90 95

Pro Gln Asn Leu Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala
100 105 110

Gln Arg Cys Asn Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp
115 120 125

```
Phe Pro Ala Val Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr
    130                 135                 140

Trp Lys Thr Ile Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Glu
145                 150                 155                 160

Asp Ala Asp Trp Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu
                165                 170                 175

Asp Asn Leu Arg Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile
            180                 185                 190

Tyr Phe Gly Arg Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser
        195                 200                 205

Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val
    210                 215                 220

Asp Ala Phe Lys Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp
225                 230                 235                 240

Leu Ala Leu Gly Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp
                245                 250                 255

Ser Arg Asp Thr Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu
            260                 265                 270

His His Leu Ile Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn
        275                 280                 285

Tyr Asn Tyr Tyr Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu
    290                 295                 300


Ala Val Ser Phe His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu
305                 310                 315                 320

Tyr Leu Val Tyr His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln
                325                 330                 335

Pro Thr Leu Pro Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys
            340                 345                 350

Asn Glu Asp Thr Lys Val Lys Leu Gly Asn Pro
        355                 360


<210> 124
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<223> Homo sapiens sialylytransferase 1

<400> 124
Ile His Thr Asn Leu Lys Lys Lys Phe Ser Cys Cys Val Leu Val Phe
  1               5                  10                  15

Leu Leu Phe Ala Val Ile Cys Val Trp Lys Glu Lys Lys Lys Gly Ser
             20                  25                  30

Tyr Tyr Asp Ser Phe Lys Leu Gln Thr Lys Glu Phe Gln Val Leu Lys
```

```
         35                  40                  45

Ser Leu Gly Lys Leu Ala Met Gly Ser Asp Ser Gln Ser Val Ser Ser
     50                  55                  60

Ser Ser Thr Gln Asp Pro His Arg Gly Arg Gln Thr Leu Gly Ser Leu
 65                  70                  75                  80

Arg Gly Leu Ala Lys Ala Lys Pro Glu Ala Ser Phe Gln Val Trp Asn
                 85                  90                  95

Lys Asp Ser Ser Ser Lys Asn Leu Ile Pro Arg Leu Gln Lys Ile Trp
            100                 105                 110

Lys Asn Tyr Leu Ser Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly Pro
        115                 120                 125

Gly Pro Gly Ile Lys Phe Ser Ala Glu Ala Leu Arg Cys His Leu Arg
    130                 135                 140

Asp His Val Asn Val Ser Met Val Glu Val Thr Asp Phe Pro Phe Asn
145                 150                 155                 160

Thr Ser Glu Trp Glu Gly Tyr Leu Pro Lys Glu Ser Ile Arg Thr Lys
                165                 170                 175

Ala Gly Pro Trp Gly Arg Cys Ala Val Val Ser Ser Ala Gly Ser Leu
            180                 185                 190

Lys Ser Ser Gln Leu Gly Arg Glu Ile Asp Asp His Asp Ala Val Leu
        195                 200                 205

Arg Phe Asn Gly Ala Pro Thr Ala Asn Phe Gln Gln Asp Val Gly Thr
    210                 215                 220

Lys Thr Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu Lys
225                 230                 235                 240

Arg Phe Leu Lys Asp Ser Leu Tyr Asn Glu Gly Ile Leu Ile Val Trp
                245                 250                 255

Asp Pro Ser Val Tyr His Ser Asp Ile Pro Lys Trp Tyr Gln Asn Pro
            260                 265                 270

Asp Tyr Asn Phe Phe Asn Asn Tyr Lys Thr Tyr Arg Lys Leu His Pro
        275                 280                 285

Asn Gln Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu Trp
    290                 295                 300

Asp Ile Leu Gln Glu Ile Ser Pro Glu Glu Ile Gln Pro Asn Pro Pro
305                 310                 315                 320

Ser Ser Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp Gln
                325                 330                 335

Val Asp Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val Cys
            340                 345                 350

Tyr Tyr Tyr Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala Tyr
        355                 360                 365

His Pro Leu Leu Tyr Glu Lys Asn Leu Val Lys His Leu Asn Gln Gly
```

```
    370                 375                 380

Thr Asp Glu Asp Ile Tyr Leu Leu Gly Lys Ala Thr Leu Pro Gly Phe
385                 390                 395                 400

Arg Thr Ile His Cys
                405
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<210> 125
<211> 518
<212> PRT
<213> Homo sapiens

<220>
<223> Homo sapiens aspartyl protease 1

<400> 125

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Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
  1               5                  10                  15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
            20                  25                  30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
        35                  40                  45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
    50                  55                  60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65                  70                  75                  80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
                85                  90                  95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
            100                 105                 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
        115                 120                 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
    130                 135                 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145                 150                 155                 160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
                165                 170                 175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
            180                 185                 190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
        195                 200                 205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
    210                 215                 220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225                 230                 235                 240
```

```
Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
                245                 250                 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
            260                 265                 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
        275                 280                 285


Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
    290                 295                 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305                 310                 315                 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
                325                 330                 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
            340                 345                 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
        355                 360                 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
    370                 375                 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385                 390                 395                 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
                405                 410                 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
            420                 425                 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
        435                 440                 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
    450                 455                 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465                 470                 475                 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
                485                 490                 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
            500                 505                 510

Val Arg His Arg Trp Lys
        515


<210> 126
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<223> Homo sapiens syntaxin 6
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<400> 126

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Met Ser Met Glu Asp Pro Phe Phe Val Val Lys Gly Glu Val Gln Lys
 1               5                  10                  15

Ala Val Asn Thr Ala Gln Gly Leu Phe Gln Arg Trp Thr Glu Leu Leu
            20                  25                  30

Gln Asp Pro Ser Thr Ala Thr Arg Glu Glu Ile Asp Trp Thr Thr Asn
        35                  40                  45

Glu Leu Arg Asn Asn Leu Arg Ser Ile Glu Trp Asp Leu Glu Asp Leu
    50                  55                  60

Asp Glu Thr Ile Ser Ile Val Glu Ala Asn Pro Arg Lys Phe Asn Leu
65                  70                  75                  80

Asp Ala Thr Glu Leu Ser Ile Arg Lys Ala Phe Ile Thr Ser Thr Arg
                85                  90                  95

Gln Val Val Arg Asp Met Lys Asp Gln Met Ser Thr Ser Ser Val Gln
            100                 105                 110

Ala Leu Ala Glu Arg Lys Asn Arg Gln Ala Leu Leu Gly Asp Ser Gly
        115                 120                 125

Ser Gln Asn Trp Ser Thr Gly Thr Thr Asp Lys Tyr Gly Arg Leu Asp
    130                 135                 140

Arg Glu Leu Gln Arg Ala Asn Ser His Phe Ile Glu Glu Gln Gln Ala
145                 150                 155                 160

Gln Gln Gln Leu Ile Val Glu Gln Gln Asp Glu Gln Leu Glu Leu Val
                165                 170                 175

Ser Gly Ser Ile Gly Val Leu Lys Asn Met Ser Gln Arg Ile Gly Gly
            180                 185                 190

Glu Leu Glu Glu Gln Ala Val Met Leu Glu Asp Phe Ser His Glu Leu
        195                 200                 205

Glu Ser Thr Gln Ser Arg Leu Asp Asn Val Met Lys Lys Leu Ala Lys
    210                 215                 220

Val Ser His Met Thr Ser Asp Arg Arg Gln Trp Cys Ala Ile Ala Ile
225                 230                 235                 240

Leu Phe Ala Val Leu Leu Val Val Leu Ile Leu Phe Leu Val Leu
                245                 250                 255
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<210> 127
<211> 1728
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid encoding recombinant fusion protein

<400> 127

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gttgaggagg agaacccgga cttctggaac cgcgaggcag ccgaggccct gggtgccgcc 120
aagaagctgc agcctgcaca gacagccgcc aagaacctca tcatcttcct gggcgatggg 180
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```
atgggggtgt ctacggtgac agctgccagg atcctaaaag ggcagaagaa ggacaaactg 240
gggcctgaga tacccctggc catggaccgc ttcccatatg tggctctgtc caagacatac 300
aatgtagaca aacatgtgcc agacagtgga gccacagcca cggcctacct gtgcggggtc 360
aagggcaact tccagaccat tggcttgagt gcagccgccc gctttaacca gtgcaacacg 420
acacgcggca acgaggtcat ctccgtgatg aatcgggcca agaaagcagg gaagtcagtg 480
ggagtggtaa ccaccacacg agtgcagcac gcctcgccag ccggcaccta cgcccacacg 540
gtgaaccgca actggtactc ggacgccgac gtgcctgcct cggcccgcca ggaggggtgc 600
caggacatcg ctacgcagct catctccaac atggacattg acgtgatcct aggtggaggc 660
cgaaagtaca tgtttcccat gggaacccca gaccctgagt acccagatga ctacagccaa 720
ggtgggacca ggctggacgg gaagaatctg gtgcaggaat ggctggcgaa gcgccagggt 780
gcccggtatg tgtggaaccg cactgagctc atgcaggctt ccctggaccc gtctgtgacc 840
catctcatgg gtctctttga gcctggagac atgaaatacg agatccaccg agactccaca 900
ctggacccct ccctgatgga gatgacagag gctgccctgc gcctgctgag caggaacccc 960
cgcggcttct tcctcttcgt ggagggtggt cgcatcgacc atggtcatca tgaaagcagg 1020
gcttaccggg cactgactga gacgatcatg ttcgacgacg ccattgagag ggcgggccag 1080
ctcaccagcg aggaggacac gctgagcctc gtcactgccg accactccca cgtcttctcc 1140
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gacaggaagg cctacacggt cctcctatac ggaaacggtc caggctatgt gctcaaggac 1260
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gcagtgcccc tggacgaaga gacccacgca ggcgaggacg tggcggtgtt cgcgcgcggc 1380
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gacgccgcgc acccaggtaa ctatgaagtt gaattccgaa gagcactcta cgtagagggt 1560
gaaagaggat tcttctacac tccaaaggca ctctacctcg tagagggtga aagaggattc 1620
ttctacacta gtctcatgac catagcctat gtcatggctg ccatctgcgc cctcttcatg 1680
ctgccactct gcctcatggt ggactacaag gatgatgatg acaagtag               1728
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<210> 128
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: recombinant
fusion protein sequence

<400> 128

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Met Leu Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu
  1               5                  10                  15

Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
             20                  25                  30

Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
         35                  40                  45

Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
     50                  55                  60

Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
 65                  70                  75                  80

Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
                 85                  90                  95

Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
            100                 105                 110

Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
        115                 120                 125

Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
    130                 135                 140
```

```
Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
145                 150                 155                 160

Gly Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
                165                 170                 175

Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
            180                 185                 190

Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
        195                 200                 205

Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met
    210                 215                 220

Phe Pro Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
225                 230                 235                 240

Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
                245                 250                 255

Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
            260                 265                 270

Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
        275                 280                 285

Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
    290                 295                 300

Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
305                 310                 315                 320

Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
                325                 330                 335

His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
            340                 345                 350

Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
        355                 360                 365

Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
    370                 375                 380

Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg
385                 390                 395                 400

Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr
                405                 410                 415

Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly
            420                 425                 430

Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr
        435                 440                 445

His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His
    450                 455                 460

Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala
465                 470                 475                 480
```

```
Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro
                485                 490                 495

Ala Gly Thr Thr Asp Ala Ala His Pro Gly Asn Tyr Glu Val Glu Pro
            500                 505                 510

Arg Arg Ala Leu Tyr Val Glu Gly Glu Arg Gly Phe Phe Tyr Thr Pro
        515                 520                 525

Lys Ala Leu Tyr Leu Val Glu Gly Glu Arg Gly Phe Phe Tyr Thr Ser
    530                 535                 540

Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met
545                 550                 555                 560

Leu Pro Leu Cys Leu Met Val Asp Tyr Lys Asp Asp Asp Asp Lys
                565                 570                 575
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<210> 129
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 129
Lys Met Asp Ala Glu
1 5

<210> 130
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 130
Gly Arg Arg Gly Ser
1 5

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 131
Val Glu Ala Asn Tyr Glu Val Glu Gly Glu
1 5 10

<210> 132
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 132
Val Glu Ala Asn Tyr Ala Val Glu Gly Glu
1 5 10

<210> 133
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 133
Lys Thr Ile Asn Leu Glu Val Glu Pro Ser
1 5 10

<210> 134
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<220>
<221> MOD_RES
<222> (5)
<223> Nle

<400> 134
Lys Thr Ile Asn Xaa Glu Val Glu Pro Ser
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (5)
<223> Nle

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 135
Lys Thr Ile Asn Xaa Glu Val Asp Pro Ser

1 5 10

<210> 136
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (5)
<223> Nle

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 136
Lys Thr Ile Asn Xaa Asp Val Asp Pro Ser
1 5 10

<210> 137
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 137
Lys Thr Ile Ser Leu Asp Val Glu Pro Ser
1 5 10

<210> 138
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 138
Lys Thr Ile Ser Leu Asp Val Asp Pro Ser
1 5 10

<210> 139
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 139
Lys Met Asp Ala
1

<210> 140
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 140
Ser Tyr Glu Val
1

<210> 141
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 141
Ser Glu Val Ser Tyr Glu Val Glu Phe Arg
1 5 10

<210> 142
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 142
Asn Leu Asp Ala
1

<210> 143
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 143
Ser Glu Val Ser Tyr Asp Ala Glu Phe Arg
1 5 10

<210> 144
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

peptide sequence

<400> 144
Ser Glu Val Ser Tyr Glu Ala Glu Phe Arg
1 5 10

<210> 145
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 145
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
1 5 10 15

Glu Val Ser Tyr Glu Val Glu Phe Arg
20 25

<210> 146
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 146
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Ser Tyr Glu
1 5 10 15

Val Glu Phe Arg
20

<210> 147
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 147
Lys Thr Glu Glu Ile Ser Glu Val Ser Tyr Glu Val Glu Phe Arg
1 5 10 15

<210> 148
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 148
Thr Glu Val Ser Tyr Glu Val Glu Phe Arg
1 5 10

<210> 149
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 149
Ser Glu Val Asp Tyr Glu Val Glu Phe Arg
1 5 10

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 150
Thr Glu Val Asp Tyr Glu Val Glu Phe Arg
1 5 10

<210> 151
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 151
Thr Glu Ile Asp Tyr Glu Val Glu Phe Arg
1 5 10

<210> 152
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 152
Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg
1 5 10

<210> 153
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 153
Ser Glu Ile Asp Tyr Glu Val Glu Phe Arg
1 5 10

<210> 154
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (11)
<223> Xaa=tryptophan

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 154
Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
1 5 10

<210> 155
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (16)
<223> Xaa=tryptophan

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 155
Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa
1 5 10 15

Lys Lys

<210> 156
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (21)
<223> Xaa=tryptophan

<220>

<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 156
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu Val
1 5 10 15

Glu Phe Arg Xaa Lys Lys
20

<210> 157
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<220>
<221> SITE
<222> (26)
<223> Xaa=tryptophan

<400> 157
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
1 5 10 15

Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
20 25

<210> 158
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (11)
<223> Xaa=tryptophan

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 158
Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
1 5 10

<210> 159
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<220>
<221> SITE

<222> (16)
<223> Xaa=tryptophan

<400> 159
Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg
1 5 10 15

Xaa Lys Lys

<210> 160
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (21)
<223> Xaa=tryptophan

<220>
<223> Description of Artificial Sequence: synthetic peptide

<400> 160
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr
1 5 10 15

Glu Val Glu Phe Arg Xaa Lys Lys
20

<210> 161
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (26)
<223> Xaa=tryptophan

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 161
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile
1 5 10 15

Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
20 25

<210> 162
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE

<222> (11)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 162
Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
1 5 10

<210> 163
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (16)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 163
Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa
1 5 10 15

Lys Lys

<210> 164
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (21)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 164
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu
1 5 10 15

Val Glu Phe Arg Xaa Lys Lys
20

<210> 165
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE

<222> (26)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 165
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
1 5 10 15

Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
20 25

<210> 166
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (11)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 166
Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
1 5 10

<210> 167
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (16)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 167
Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg
1 5 10 15

Xaa Lys Lys

<210> 168
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

<221> SITE
<222> (21)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 168
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr
1 5 10 15

Glu Val Glu Phe Arg Xaa Lys Lys
20

<210> 169
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (26)
<223> Xaa=oregon green

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 169
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile
1 5 10 15

Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Xaa Lys Lys
20 25

<210> 170
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide sequence

<400> 170
Ser Glu Val Asn Tyr Glu Val Glu Phe Arg
1 5 10

<210> 171
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer for site-directed mutagenesis of APP

<400> 171
gagatctctg aaattagtta tgaagtagaa ttccgacatg actcagg 47

<210> 172
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for site-directed mutagenesis of APP

<400> 172
tgagtcatgt cggaattcta cttcataact aatttcagag atctcctc 48

<210> 173
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for site-directed mutagenesis of APP

<400> 173
gagatctctg aaagtagtta tgaagtagaa ttccgacatg actcagg 47

<210> 174
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for site-directed mutagenesis of APP

<400> 174
tgagtcatgt cggaattcta cttcataact actttcagag atctcctc 48

<210> 175
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for site-directed mutagenesis of APP

<400> 175
gagatctctg aaattagtta tgaagcagaa ttccgacatg actcagg 47

<210> 176
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for site-directed mutagenesis of APP

<400> 176
tgagtcatgt cggaattctg cttcataact aatttcagag atctcctc 48

<210> 177
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 177
Val Ser Tyr Glu Val
1 5

<210> 178
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 178
Val Ser Tyr Asp Ala
1 5

<210> 179
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 179
Ile Ser Tyr Glu Val
1 5

<210> 180
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 180
Val Lys Met Asp Ala
1 5

<210> 181
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for generating mutant construct named MBPC125-SYEV

<400> 181
gacatctctg aagtgagtta ttaggcagaa ttccgacatg actcagg 47

<210> 182
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic primer for generating mutant construct named MBPC125-SYEV

<400> 182
tgagtcatgt cggaattctg cctaataact cacttcagag atctcctc 48

<210> 183
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 183
Lys Lys Ser Tyr Glu Val
1 5

<210> 184
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 184
Val Glu Ala Asn Tyr Glu Val Glu Gly Glu
1 5 10

<210> 185
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 185
Val Glu Ala Asn Tyr Ala Val Glu Gly Glu
1 5 10

<210> 186
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 186
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 187
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 187
Ser Tyr Glu Ala
1

<210> 188
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 188
Ser Tyr Ala Val
1

<210> 189
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide sequence

<400> 189
Val Ser Tyr Glu Ala
1 5

<210> 190

<211> 13

<212> PRT

<213> synthetic peptide sequence

<400> 190

Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Trp Lys Lys
1 5 10

<210> 191

<211> 23

<212> PRT

<213> synthetic peptide sequence

<400> 191

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu
1 5 10 15

Val Glu Phe Arg Trp Lys Lys
20

<210> 192

<211> 15

<212> PRT

<213> synthetic peptide sequence

<220>

<221> SITE

<222> (1)..(1)

<223> amino acid at position 1 is biotinylated

<220>

<221> SITE

<222> (14)..(14)

<223> cys at position 14 is derivatized with an oregon green

<400> 192

Lys Glu Ile Ser Glu Ile Ser Tyr Glu Val Glu Phe Arg Lys Lys
1 5 10 15

<210> 193

<211> 22

<212> PRT

<213> synthetic peptide sequence

<220>

<221> SITE

<222> (1)..(1)

<223> amino acid at position 1 is biotinylated

<220>

<221> SITE

<222> (21)..(21)

<223> cys at position 21 is derivatized with an oregon green

<400> 193

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Ile Ser Tyr Glu
1 5 10 15

Val Glu Phe Arg Lys Lys
20

<210> 194

<211> 6806

<212> DNA

<213> fusion protein comprising a maltose binding protein with 125 amino acids from APP C-terminus.

<400> 194

ccgacaccat cgaatggcgc aaaacctttc gcggtatggc atgatagcgc ccggaagaga 60

gtcaattcag ggtggtgaat gtgaaaccag taacgttata cgatgtcgca gagtatgccg 120

gtgtctctta tcagaccgtt tcccgcgtgg tgaaccaggc cagccacgtt tctgcgaaaa 180

cgcgggaaaa agtggaagcg gcgatggcgg agctgaatta cattcccaac cgcgtggcac 240

aacaactggc gggcaaacag tcgttgctga ttggcgttgc cacctccagt ctggccctgc 300

acgcgccgtc gcaaattgtc gcggcgatta aatctcgcgc cgatcaactg ggtgccagcg 360

tggtggtgtc gatggtagaa cgaagcggcg tcgaagcctg taaagcggcg gtgcacaatc 420

ttctcgcgca acgcgtcagt gggctgatca ttaactatcc gctggatgac caggatgcca 480

ttgctgtgga agctgcctgc actaatgttc cggcgttatt tcttgatgtc tctgaccaga 540

cacccatcaa cagtattatt ttctcccatg aagacggtac gcgactgggc gtggagcatc 600

tggtcgcatt gggtcaccag caaatcgcgc tgttagcggg cccattaagt tctgtctcgg 660

cgcgtctgcg tctggctggc tggcataaat atctcactcg caatcaaatt cagccgatag 720

cggaacggga aggcgactgg agtgccatgt ccggttttca acaaaccatg caaatgctga 780

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gcctgctggg gcaaaccagc gtggaccgct tgctgcaact ctctcagggc caggcggtga 1020

agggcaatca gctgttgccc gtctcactgg tgaaaagaaa aaccaccctg gcgcccaata 1080

cgcaaaccgc ctctccccgc gcgttggccg attcattaat gcagctggca cgacaggttt 1140

cccgactgga aagcgggcag tgagcgcaac gcaattaatg tgagttagct cactcattag 1200

gcacaattct catgtttgac agcttatcat cgactgcacg gtgcaccaat gcttctggcg 1260

tcaggcagcc atcggaagct gtggtatggc tgtgcaggtc gtaaatcact gcataattcg 1320

tgtcgctcaa ggcgcactcc cgttctggat aatgtttttt gcgccgacat cataacggtt 1380

ctggcaaata ttctgaaatg agctgttgac aattaatcat cggctcgtat aatgtgtgga 1440

attgtgagcg gataacaatt tcacacagga aacagccagt ccgtttaggt gttttcacga 1500

gcacttcacc aacaaggacc atagattatg aaaactgaag aaggtaaact ggtaatctgg 1560

attaacggcg ataaaggcta taacggtctc gctgaagtcg gtaagaaatt cgagaaagat 1620

accggaatta aagtcaccgt tgagcatccg gataaactgg aagagaaatt cccacaggtt 1680

gcggcaactg gcgatggccc tgacattatc ttctgggcac acgaccgctt tggtggctac 1740

gctcaatctg gcctgttggc tgaaatcacc ccggacaaag cgttccagga caagctgtat 1800

ccgtttacct gggatgccgt acgttacaac ggcaagctga ttgcttaccc gatcgctgtt 1860

gaagcgttat cgctgattta taacaaagat ctgctgccga acccgccaaa aacctgggaa 1920

gagatcccgg cgctggataa agaactgaaa gcgaaaggta agagcgcgct gatgttcaac 1980

ctgcaagaac cgtacttcac ctggccgctg attgctgctg acgggggtta tgcgttcaag 2040

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ggtctgacct tcctggttga cctgattaaa aacaaacaca tgaatgcaga caccgattac 2160

tccatcgcag aagctgcctt taataaaggc gaaacagcga tgaccatcaa cggcccgtgg 2220

gcatggtcca acatcgacac cagcaaagtg aattatggtg taacggtact gccgaccttc 2280

aagggtcaac catccaaacc gttcgttggc gtgctgagcg caggtattaa cgccgccagt 2340

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tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc 2760

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 2820

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gtggaggttg acgccgctgt caccccagag gagcgccacc tgtccaagat gcagcagaac 3000

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactagac ccccgccaca 3060

gcagcctctg aagttggaca gcaaaaccat tgcttcacta cccatcggtg tccatttata 3120

gaataatgtg ggaagaaaca aacccgtttt atgatttact cattatcgcc ttttgacagc 3180

tgtgctgtaa cacaagtaga tgcctgaact tgaattaatc cacacatcag taatgtattc 3240

tatctctctt tacattttgg tctctatact acattattaa tgggttttgt gtactgtaaa 3300

gaatttagct gtatcaaact agtaatagcc tgaattcagt aacctaaccc tcgatggatc 3360

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gcgtaatagc gaagaggccc gcaccgatcg cccttcccaa cagttgcgca gcctgaatgg 3540

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gtctccccat gcgagagtag ggaactgcca ggcatcaaat aaaacgaaag gctcagtcga 3780

aagactgggc ctttcgtttt atctgttgtt tgtcggtgaa cgctctcctg agtaggacaa 3840

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gcccgccata aactgccagg catcaaatta agcagaaggc catcctgacg gatggccttt 3960

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catgagacaa taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat 4080

tcaacatttc cgtgtcgccc ttattccctt ttttgcggca ttttgccttc ctgtttttgc 4140

tcacccagaa acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg 4200

ttacatcgaa ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg 4260

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ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctgtagc 4620

aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca 4680

acaattaata gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct 4740

tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat 4800

cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg 4860

gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat 4920

taagcattgg taactgtcag accaagttta ctcatatata ctttagattg atttaaaact 4980

tcatttttaa tttaaaagga tctaggtgaa gatccttttt gataatctca tgaccaaaat 5040

cccttaacgt gagttttcgt tccactgagc gtcagacccc gtagaaaaga tcaaaggatc 5100

ttcttgagat cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct 5160

accagcggtg gtttgtttgc cggatcaaga gctaccaact ctttttccga aggtaactgg 5220

cttcagcaga gcgcagatac caaatactgt ccttctagtg tagccgtagt taggccacca 5280

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<212> PRT

<213> synthetic peptide sequence

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<221> MOD_RES

<222> (1)..(1)

<223> ACETYLATION (MCA)

<220>

<221> SITE

<222> (11)..(11)

<223> 2,4-dinitrophenyl group after the Lys at position 11

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<222> (4)..(4)

<223> amino acid at position 4 has been derivatized with a statine

<400> 196

Ser Glu Val Asn Val Ala Glu Phe Arg Gly Gly Cys
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<222> (4)..(4)

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<222> (10)..(10)

<223> amino acid at position 10 has been derivatized with Bodipy FL

<400> 197

Ser Glu Val Asn Val Ala Glu Phe Arg Cys
1 5 10